

5/06/03 odjaisly



1600

RAW SEQUENCE LISTING

DATE: 01/29/2003

PATENT APPLICATION: US/09/712,768A

TIME: 19:32:41

#12

Input Set : N:\Crf4\Refhold\I712768A.raw

Output Set: N:\CRF4\01292003\I712768A.raw

ENTERED

C--> 1 <110> APPLICANT: Asakura, Akira
 2 Hoshino, Tatsuo
 3 Shinjoh, Masako
 4 <120> TITLE OF INVENTION: Cytochrome C Oxidase Enzyme Complex
 5 <130> FILE REFERENCE: C38435/111693
 6 <140> CURRENT APPLICATION NUMBER: US/09/712,768A
 7 <141> CURRENT FILING DATE: 2002-11-13
 8 <150> PRIOR APPLICATION NUMBER: EP 99122842
 9 <151> PRIOR FILING DATE: 1999-11-17
 10 <160> NUMBER OF SEQ ID NOS: 36
 11 <170> SOFTWARE: PatentIn version 3.1
 13 <210> SEQ ID NO: 1
 14 <211> LENGTH: 1674
 15 <212> TYPE: DNA
 16 <213> ORGANISM: Gluconobacter oxydans
 17 <220> FEATURE:
 18 <221> NAME/KEY: CDS
 19 <222> LOCATION: (1)..(1674)
 20 <223> OTHER INFORMATION:

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25	ttc ttc acg cgc tgg ttc atg tcg acc aac cac aaa gac atc ggt ctg	96
26	Phe Phe Thr Arg Trp Phe Met Ser Thr Asn His Lys Asp Ile Gly Leu	
27	20 25 30	
28	cta tac ctt gta gcg gct ggt gtt gtt ggt ttc att tcc gtc ctg ttc	144
29	Leu Tyr Leu Val Ala Ala Gly Val Val Gly Phe Ile Ser Val Leu Phe	
30	35 40 45	
31	acc gtc tac atg cgc ctt gag ctg atg gat ccg ggt gtt cag tac atg	192
32	Thr Val Tyr Met Arg Leu Glu Leu Met Asp Pro Gly Val Gln Tyr Met	
33	50 55 60	
34	tgc ctt gaa ggc gca cgt ctg atc gcg gat gcc tcg cag aca tgt acg	240
35	Cys Leu Glu Gly Ala Arg Leu Ile Ala Asp Ala Ser Gln Thr Cys Thr	
36	65 70 75 80	
37	gcg aac gga cac ctg tgg aac gtc atg gtt acc tac cat ggt att ctg	288
38	Ala Asn Gly His Leu Trp Asn Val Met Val Thr Tyr His Gly Ile Leu	
39	85 90 95	
40	atg atg ttc ttt gtg ggt atc ccc gca ttg ttc ggt ggt ttt ggt aac	336
41	Met Met Phe Phe Val Gly Ile Pro Ala Leu Phe Gly Gly Phe Gly Asn	
42	100 105 110	
43	tat ctg atg ccg ctg caa atc ggc gct ccg gat atg gcc ttc ccg cgt	384
44	Tyr Leu Met Pro Leu Gln Ile Gly Ala Pro Asp Met Ala Phe Pro Arg	

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94      ggt ggt gtg acc ggt atc gtg ctg gcc caa gcg ggt ctg gac cgt gca      1200
95      Gly Gly Val Thr Gly Ile Val Leu Ala Gln Ala Gly Leu Asp Arg Ala
96      385                      390                      395                      400
97      tat cac gac acc tat tac gtg gtg gcg cac ttc cat tat gtg atg tcg      1248
98      Tyr His Asp Thr Tyr Tyr Val Val Ala His Phe His Tyr Val Met Ser
99                      405                      410                      415
100     ctg ggt gcg atc ttt gcg atc ttc gcc ggt atc tac ttt tac atg ccg      1296
101     Leu Gly Ala Ile Phe Ala Ile Phe Ala Gly Ile Tyr Phe Tyr Met Pro
102                      420                      425                      430
103     aag ttc tcg ggc cgc gct ttc ccg gaa tgg gct gca aag ctg cac ttc      1344
104     Lys Phe Ser Gly Arg Ala Phe Pro Glu Trp Ala Ala Lys Leu His Phe
105                      435                      440                      445
106     tgg acc ttc ttc atc ggt gcg aac gtc acg ttc ttc ccg cag cac ttc      1392
107     Trp Thr Phe Phe Ile Gly Ala Asn Val Thr Phe Phe Pro Gln His Phe
108                      450                      455                      460
109     ctg gga cgt cag ggt atg ccg cgc cgt tac atc gac tat ccc gaa gcc      1440
110     Leu Gly Arg Gln Gly Met Pro Arg Arg Tyr Ile Asp Tyr Pro Glu Ala
111     465                      470                      475                      480
112     ttc gcg ctg tgg aac aaa gtc tcg tcc tat ggt gcg ttc ctg gcc ttc      1488
113     Phe Ala Leu Trp Asn Lys Val Ser Ser Tyr Gly Ala Phe Leu Ala Phe
114                      485                      490                      495
115     gcc tcg ttc ctg ttc ttc atc gtg atc ttt gtc tat acg ctg gtt gct      1536
116     Ala Ser Phe Leu Phe Phe Ile Val Ile Phe Val Tyr Thr Leu Val Ala
117                      500                      505                      510
118     ggc cgc cgc gag acc cgt ccg aac ccg tgg ggc gaa ttc gcc gat acg      1584
119     Gly Arg Arg Glu Thr Arg Pro Asn Pro Trp Gly Glu Phe Ala Asp Thr
120                      515                      520                      525
121     ctg gaa tgg acg ctg cca tca ccg cct ccg gcc cac acg ttc gaa acg      1632
122     Leu Glu Trp Thr Leu Pro Ser Pro Pro Pro Ala His Thr Phe Glu Thr
123                      530                      535                      540
124     ctg ccc aag cgc tcg gac tgg gac aag cat ccc tcg cac taa      1674
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128 <210> SEQ ID NO: 2
129 <211> LENGTH: 557
130 <212> TYPE: PRT
131 <213> ORGANISM: Gluconobacter oxydans
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136                      20                      25                      30
137     Leu Tyr Leu Val Ala Ala Gly Val Val Gly Phe Ile Ser Val Leu Phe
138                      35                      40                      45
139     Thr Val Tyr Met Arg Leu Glu Leu Met Asp Pro Gly Val Gln Tyr Met
140                      50                      55                      60
141     Cys Leu Glu Gly Ala Arg Leu Ile Ala Asp Ala Ser Gln Thr Cys Thr
142     65                      70                      75                      80
143     Ala Asn Gly His Leu Trp Asn Val Met Val Thr Tyr His Gly Ile Leu

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144				85				90				95
145	Met	Met	Phe	Phe	Val	Gly	Ile	Pro	Ala	Leu	Phe	Gly
146				100					105			110
147	Tyr	Leu	Met	Pro	Leu	Gln	Ile	Gly	Ala	Pro	Asp	Met
148				115					120			125
149	Met	Asn	Asn	Leu	Ser	Phe	Trp	Leu	Phe	Ile	Ala	Gly
150				130					135			140
151	Val	Ala	Ser	Leu	Phe	Ala	Pro	Gly	Gly	Asp	Gly	Gln
152												155
153	Val	Gly	Trp	Val	Leu	Tyr	Pro	Pro	Leu	Ser	Thr	Arg
154												160
155	Ser	Met	Asp	Leu	Ala	Ile	Phe	Ala	Val	His	Leu	Ser
156				165					170			175
157	Ile	Met	Gly	Ala	Ile	Asn	Met	Ile	Thr	Thr	Phe	Leu
158				180					185			190
159	Pro	Gly	Met	Thr	Leu	His	Lys	Val	Pro	Leu	Phe	Ser
160				195					200			205
161	Ile	Thr	Ala	Trp	Leu	Ile	Leu	Leu	Ala	Leu	Pro	Val
162												210
163	Ile	Thr	Met	Leu	Leu	Thr	Asp	Arg	Asn	Phe	Gly	Thr
164				225					230			235
165	Pro	Ala	Gly	Gly	Gly	Asp	Pro	Ile	Leu	Tyr	Gln	His
166				245					250			255
167	Phe	Gly	His	Pro	Glu	Val	Tyr	Ile	Ile	Ile	Leu	Pro
168				260					265			270
169	Ile	Ser	His	Val	Val	Ser	Thr	Phe	Ser	Lys	Lys	Pro
170				275					280			285
171	Leu	Pro	Met	Val	Tyr	Ala	Met	Val	Ala	Ile	Gly	Val
172				290					295			300
173	Val	Trp	Ala	His	His	Met	Tyr	Thr	Val	Gly	Met	Ser
174				305					310			315
175	Ser	Tyr	Phe	Met	Leu	Ala	Thr	Met	Val	Ile	Ala	Val
176				325					330			335
177	Lys	Ile	Phe	Ser	Trp	Ile	Ala	Thr	Met	Trp	Gly	Gly
178				340					345			350
179	Lys	Ser	Pro	Met	Leu	Trp	Ala	Phe	Gly	Phe	Met	Phe
180				355					360			365
181	Gly	Gly	Val	Thr	Gly	Ile	Val	Leu	Ala	Gln	Ala	Gly
182				370					375			380
183	Tyr	His	Asp	Thr	Tyr	Tyr	Val	Val	Ala	His	Phe	His
184				385					390			395
185	Leu	Gly	Ala	Ile	Phe	Ala	Ile	Phe	Ala	Gly	Ile	Tyr
186				405					410			415
187	Lys	Phe	Ser	Gly	Arg	Ala	Phe	Pro	Glu	Trp	Ala	Ala
188				420					425			430
189	Trp	Thr	Phe	Phe	Ile	Gly	Ala	Asn	Val	Thr	Phe	Phe
190				435					440			445
191	Leu	Gly	Arg	Gln	Gly	Met	Pro	Arg	Arg	Tyr	Ile	Asp
192				450					455			460
				465					470			475
												480

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Input Set : N:\Crf4\Refhold\I712768A.raw

Output Set: N:\CRF4\01292003\I712768A.raw

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193   Phe Ala Leu Trp Asn Lys Val Ser Ser Tyr Gly Ala Phe Leu Ala Phe
194           485           490           495
195   Ala Ser Phe Leu Phe Phe Ile Val Ile Phe Val Tyr Thr Leu Val Ala
196           500           505           510
197   Gly Arg Arg Glu Thr Arg Pro Asn Pro Trp Gly Glu Phe Ala Asp Thr
198           515           520           525
199   Leu Glu Trp Thr Leu Pro Ser Pro Pro Pro Ala His Thr Phe Glu Thr
200           530           535           540
201   Leu Pro Lys Arg Ser Asp Trp Asp Lys His Pro Ser His
202           545           550           555
204 <210> SEQ ID NO: 3
205 <211> LENGTH: 132
206 <212> TYPE: DNA
207 <213> ORGANISM: Gluconobacter oxydans
208 <220> FEATURE:
209 <221> NAME/KEY: CDS
210 <222> LOCATION: (1)..(132)
211 <223> OTHER INFORMATION:
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214   Pro Leu Glu Ile Val Trp Thr Ile Val Pro Val Val Ile Leu Val Phe
215   1           5           10           15
216   atc ggt gcg ttc tcg ctg ccg gtg ctg ttc aaa cag caa gag ttc ccc      96
217   Ile Gly Ala Phe Ser Leu Pro Val Leu Phe Lys Gln Gln Glu Phe Pro
218   20           25           30
219   gag ggt gac atc gtc atc aac gtc gag ggt cgt agc      132
220   Glu Gly Asp Ile Val Ile Asn Val Glu Gly Arg Ser
221   35           40
223 <210> SEQ ID NO: 4
224 <211> LENGTH: 44
225 <212> TYPE: PRT
226 <213> ORGANISM: Gluconobacter oxydans
227 <400> SEQUENCE: 4
228   Pro Leu Glu Ile Val Trp Thr Ile Val Pro Val Val Ile Leu Val Phe
229   1           5           10           15
230   Ile Gly Ala Phe Ser Leu Pro Val Leu Phe Lys Gln Gln Glu Phe Pro
231   20           25           30
232   Glu Gly Asp Ile Val Ile Asn Val Glu Gly Arg Ser
233   35           40
235 <210> SEQ ID NO: 5
236 <211> LENGTH: 114
237 <212> TYPE: DNA
238 <213> ORGANISM: Gluconobacter oxydans
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242 <223> OTHER INFORMATION:
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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/712,768A

DATE: 01/29/2003
TIME: 19:32:42

Input Set : N:\Crf4\Refhold\I712768A.raw
Output Set: N:\CRF4\01292003\I712768A.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:31; N Pos. 12
Seq#:32; N Pos. 3,9
Seq#:33; N Pos. 9
Seq#:34; N Pos. 12
Seq#:35; N Pos. 3,9
Seq#:36; N Pos. 18